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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/930,020A

DATE: 05/01/2002

TIME: 09:21:25

Input Set : A:\18501-31.app

Output Set: N:\CRF3\05012002\I930020A.raw

3 <110> APPLICANT: Gish, Kurt C.
 4 Mack, David H.
 5 Wilson, Keith E.
 6 Eos Biotechnology, Inc.
 8 <120> TITLE OF INVENTION: Methods of Diagnosis of Colorectal Cancer, Compositions
 9 and Methods of Screening for Colorectal Cancer
 10 Modulators
 12 <130> FILE REFERENCE: 018501-003100US
 14 <140> CURRENT APPLICATION NUMBER: US 09/930,020A
 15 <141> CURRENT FILING DATE: 2001-08-14
 17 <150> PRIOR APPLICATION NUMBER: US 09/663,733
 18 <151> PRIOR FILING DATE: 2000-09-15
 20 <160> NUMBER OF SEQ ID NOS: 3
 22 <170> SOFTWARE: PatentIn Ver. 2.1
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 3375
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Homo sapiens
 29 <220> FEATURE:
 30 <223> OTHER INFORMATION: CBF9
 32 <220> FEATURE:
 33 <221> NAME/KEY: CDS
 34 <222> LOCATION: (328)..(2751)
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 40 cctggcggtt gttccctccga cctcagccgg gtcgggtcggt gcccgcctct cccaggagag 180
 41 acaaaacaggt gtcccacgtg gcagccgcgc cccggcgcc cctcctgtga tcccgtagcg 240
 42 cccccctggcc cgagccgcgc cccgggtctgt gagtagagcc gcccgggcac cgagcgctgg 300
 43 tcgcccgtct cttccgttatacacatg cccctttcc ttgtgttggg ggccgtctgt 360
 44 gttttccgtt tttccagagt gccccatct ctcctctcc aggaagtcca tgtaagcaaa 420
 45 gaaaccatcg ggaagatttc agctgccagc aaaatgtatgt ggtgctcggc tgcagtggac 480
 46 atcatgttcc ttgttagatgg gtctaacagc gtcggaaaag ggagctttga aagggtccaaag 540
 47 cactttgcca tcacagtctg tgacggctctg gacatcagcc ccggaggggt cagagtggg 600
 48 gcattccagt tcagttccac tcctcatctg gaattccctt tggattcatt ttcaacccaa 660
 49 caggaagtga aggcaagaat caagaggatg gtttcaaag gagggcgcac ggagacggaa 720
 50 cttgtctctga aatacccttgc acacagagggtt gtcgttgggg gcagaaaatgc ttctgtgccc 780
 51 cagatcctca tcacgttcac tgatggaaatg tcccaggggg atgtggcact gccatccaag 840
 52 cagctgaagg aaagggtgt cactgtgttt gctgtgggg tcaggtttcc caggtgggag 900
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56 gagttcgctg gcaatcccc atgctggaga ggatcgccgc ggacccttgc ggtgctggct 1140
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 58 aggaccacct gcccaggccc ctgtgactcg cagccctgcc agaatggagg cacatgtgtt 1260
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 61 gcccccacca ctctggacgg cttcctgcgg gccaaagtct tcgtgaagcg gtttgcgg 1440
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 98 <211> LENGTH: 807
 99 <212> TYPE: PRT
 100 <213> ORGANISM: Homo sapiens
 102 <220> FEATURE:
 103 <223> OTHER INFORMATION: CBF9
 105 <400> SEQUENCE: 2
 106 Met Pro Pro Phe Leu Leu Leu Glu Ala Val Cys Val Phe Leu Phe Ser
 107 1 5 10 15
 108 Arg Val Pro Pro Ser Leu Pro Leu Gln Glu Val His Val Ser Lys Glu

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109	20	25	30	
110	Thr Ile Gly Lys Ile Ser Ala Ala Ser Lys Met Met Trp Cys Ser Ala			
111	35	40	45	
112	Ala Val Asp Ile Met Phe Leu Leu Asp Gly Ser Asn Ser Val Gly Lys			
113	50	55	60	
114	Gly Ser Phe Glu Arg Ser Lys His Phe Ala Ile Thr Val Cys Asp Gly			
115	65	70	75	80
116	Leu Asp Ile Ser Pro Glu Arg Val Arg Val Gly Ala Phe Gln Phe Ser			
117	85	90	95	
118	Ser Thr Pro His Leu Glu Phe Pro Leu Asp Ser Phe Ser Thr Gln Gln			
119	100	105	110	
120	Glu Val Lys Ala Arg Ile Lys Arg Met Val Phe Lys Gly Gly Arg Thr			
121	115	120	125	
122	Glu Thr Glu Leu Ala Leu Lys Tyr Leu Leu His Arg Gly Leu Pro Gly			
123	130	135	140	
124	Gly Arg Asn Ala Ser Val Pro Gln Ile Leu Ile Ile Val Thr Asp Gly			
125	145	150	155	160
126	Lys Ser Gln Gly Asp Val Ala Leu Pro Ser Lys Gln Leu Lys Glu Arg			
127	165	170	175	
128	Gly Val Thr Val Phe Ala Val Gly Val Arg Phe Pro Arg Trp Glu Glu			
129	180	185	190	
130	Leu His Ala Leu Ala Ser Glu Pro Arg Gly Gln His Val Leu Leu Ala			
131	195	200	205	
132	Glu Gln Val Glu Asp Ala Thr Asn Gly Leu Phe Ser Thr Leu Ser Ser			
133	210	215	220	
134	Ser Ala Ile Cys Ser Ser Ala Thr Pro Asp Cys Arg Val Glu Ala His			
135	225	230	235	240
136	Pro Cys Glu His Arg Thr Leu Glu Met Val Arg Glu Phe Ala Gly Asn			
137	245	250	255	
138	Ala Pro Cys Trp Arg Gly Ser Arg Arg Thr Leu Ala Val Leu Ala Ala			
139	260	265	270	
140	His Cys Pro Phe Tyr Ser Trp Lys Arg Val Phe Leu Thr His Pro Ala			
141	275	280	285	
142	Thr Cys Tyr Arg Thr Thr Cys Pro Gly Pro Cys Asp Ser Gln Pro Cys			
143	290	295	300	
144	Gln Asn Gly Gly Thr Cys Val Pro Glu Gly Leu Asp Gly Tyr Gln Cys			
145	305	310	315	320
146	Leu Cys Pro Leu Ala Phe Gly Gly Glu Ala Asn Cys Ala Leu Lys Leu			
147	325	330	335	
148	Ser Leu Glu Cys Arg Val Asp Leu Leu Phe Leu Leu Asp Ser Ser Ala			
149	340	345	350	
150	Gly Thr Thr Leu Asp Gly Phe Leu Arg Ala Lys Val Phe Val Lys Arg			
151	355	360	365	
152	Phe Val Arg Ala Val Leu Ser Glu Asp Ser Arg Ala Arg Val Gly Val			
153	370	375	380	
154	Ala Thr Tyr Ser Arg Glu Leu Leu Val Ala Val Pro Val Gly Glu Tyr			
155	385	390	395	400
156	Gln Asp Val Pro Asp Leu Val Trp Ser Leu Asp Gly Ile Pro Phe Arg			
157	405	410	415	

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158 Gly Gly Pro Thr Leu Thr Gly Ser Ala Leu Arg Gln Ala Ala Glu Arg
159 420 425 430
160 Gly Phe Gly Ser Ala Thr Arg Thr Gly Gln Asp Arg Pro Arg Arg Val
161 435 440 445
162 Val Val Leu Leu Thr Glu Ser His Ser Glu Asp Glu Val Ala Gly Pro
163 450 455 460
164 Ala Arg His Ala Arg Ala Arg Glu Leu Leu Leu Gly Val Gly Ser
165 465 470 475 480
166 Glu Ala Val Arg Ala Glu Leu Glu Glu Ile Thr Gly Ser Pro Lys His
167 485 490 495
168 Val Met Val Tyr Ser Asp Pro Gln Asp Leu Phe Asn Gln Ile Pro Glu
169 500 505 510
170 Leu Gln Gly Lys Leu Cys Ser Arg Gln Arg Pro Gly Cys Arg Thr Gln
171 515 520 525
172 Ala Leu Asp Leu Val Phe Met Leu Asp Thr Ser Ala Ser Val Gly Pro
173 530 535 540
174 Glu Asn Phe Ala Gln Met Gln Ser Phe Val Arg Ser Cys Ala Leu Gln
175 545 550 555 560
176 Phe Glu Val Asn Pro Asp Val Thr Gln Val Gly Leu Val Val Tyr Gly
177 565 570 575
178 Ser Gln Val Gln Thr Ala Phe Gly Leu Asp Thr Lys Pro Thr Arg Ala
179 580 585 590
180 Ala Met Leu Arg Ala Ile Ser Gln Ala Pro Tyr Leu Gly Gly Val Gly
181 595 600 605
182 Ser Ala Gly Thr Ala Leu Leu His Ile Tyr Asp Lys Val Met Thr Val
183 610 615 620
184 Gln Arg Gly Ala Arg Pro Gly Val Pro Lys Ala Val Val Val Leu Thr
185 625 630 635 640
186 Gly Gly Arg Gly Ala Glu Asp Ala Ala Val Pro Ala Gln Lys Leu Arg
187 645 650 655
188 Asn Asn Gly Ile Ser Val Leu Val Val Gly Val Gly Pro Val Leu Ser
189 660 665 670
190 Glu Gly Leu Arg Arg Leu Ala Gly Pro Arg Asp Ser Leu Ile His Val
191 675 680 685
192 Ala Ala Tyr Ala Asp Leu Arg Tyr His Gln Asp Val Leu Ile Glu Trp
193 690 695 700
194 Leu Cys Gly Glu Ala Lys Gln Pro Val Asn Leu Cys Lys Pro Ser Pro
195 705 710 715 720
196 Cys Met Asn Glu Gly Ser Cys Val Leu Gln Asn Gly Ser Tyr Arg Cys
197 725 730 735
198 Lys Cys Arg Asp Gly Trp Glu Gly Pro His Cys Glu Asn Arg Glu Trp
199 740 745 750
200 Ser Ser Cys Ser Val Cys Val Ser Gln Gly Trp Ile Leu Glu Thr Pro
201 755 760 765
202 Leu Arg His Met Ala Pro Val Gln Glu Gly Ser Ser Arg Thr Pro Pro
203 770 775 780
204 Ser Asn Tyr Arg Glu Gly Leu Gly Thr Glu Met Val Pro Thr Phe Trp
205 785 790 795 800
206 Asn Val Cys Ala Pro Gly Pro

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Input Set : A:\18501-31.app
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207 805
210 <210> SEQ ID NO: 3
211 <211> LENGTH: 5
212 <212> TYPE: PRT
213 <213> ORGANISM: Artificial Sequence
215 <220> FEATURE:
216 <223> OTHER INFORMATION: Description of Artificial Sequence:conserved
217 cytokine receptor extracellular motif
219 <220> FEATURE:
220 <221> NAME/KEY: MOD_RES
221 <222> LOCATION: (3)
222 <223> OTHER INFORMATION: Xaa = any amino acid
224 <400> SEQUENCE: 3
W--> 225 Trp Ser Xaa Trp Ser
226 1 5

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/930,020A

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Input Set : A:\18501-31.app
Output Set: N:\CRF3\05012002\I930020A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; Xaa Pos. 3

VERIFICATION SUMMARY
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Input Set : A:\18501-31.app
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L:225 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0